

RW

PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/868,605

DATE: 07/05/2001

TIME: 15:38:31

Input Set : A:\PTO.txt

Output Set: N:\CRF3\07032001\I868605.raw

3 <110> APPLICANT: ML Laboratories PLC
 5 <120> TITLE OF INVENTION: Immunosuppression
 7 <130> FILE REFERENCE: P15700WO
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/868,605
 C--> 10 <141> CURRENT FILING DATE: 2001-06-19
 12 <150> PRIOR APPLICATION NUMBER: 9827921.9
 13 <151> PRIOR FILING DATE: 1998-12-19
 15 <150> PRIOR APPLICATION NUMBER: 9925015.1
 16 <151> PRIOR FILING DATE: 1999-10-23
 18 <160> NUMBER OF SEQ ID NOS: 39
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 288
 24 <212> TYPE: PRT
 25 <213> ORGANISM: Homo sapiens
 27 <400> SEQUENCE: 1
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 32 20 25 30
 34 Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
 35 35 40 45
 37 Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
 38 50 55 60
 40 Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
 41 65 70 75 80
 43 Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
 44 85 90 95
 46 Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
 47 100 105 110
 49 Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
 50 115 120 125
 52 Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
 53 130 135 140
 55 Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
 56 145 150 155 160
 58 Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
 59 165 170 175
 61 Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
 62 180 185 190
 64 Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met
 65 195 200 205
 67 Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg
 68 210 215 220
 70 Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro
 71 225 230 235 240
 73 Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly

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74          245          250          255
76 Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg
77          260          265          270
79 Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
80          275          280          285
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87 <211> LENGTH: 972
88 <212> TYPE: DNA
89 <213> ORGANISM: Homo sapiens
91 <400> SEQUENCE: 2
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93 aagattcaag cttattttcaa tgagactgca gacctgccat gccaatattgc aaactctcaa 120
94 aaccaaagcc tgagtgaagt agtagtattt tggcaggacc aggaaaactt ggttctgaat 180
95 gaggtatact taggcaaaga gaaatttgac agtgttcatt ccaagtatat gggccgcaca 240
96 agttttgatt cggacagttg gacctgaga cttcacaatc ttcagatcaa ggacaagggc 300
97 ttgtatcaat gtatcatcca tcacaaaaag cccacaggaa tgattcgcac ccaccagatg 360
98 aattctgaac tgtcagtgct tgctaacttc agtcaacctg aaatagtacc aatttctaata 420
99 ataacagaaa atgtgtacat aaatttgacc tgctcatcta tacacgggta cccagaacct 480
100 aagaagatga gtgttttgct aagaaccaag aattcaacta tcgagtatga tggattattg 540
101 cagaaatctc aagataatgt cacagaactg tacgacgttt ccatcagctt gtctgtttca 600
102 ttccctgatg ttacgagcaa tatgaccatc ttctgtatct tggaaactga caagacgcgg 660
103 cttttatctt cacctttctc tatagagctt gaggaccctc agcctcccc agaccacatt 720
104 ccttgatta cagctgtact tccaacagtt attatatgtg tgatggtttt ctgtctaatt 780
105 ctatggaaat ggaagaagaa gaagcggcct cgcaactctt ataaatgtgg aaccaacaca 840
106 atggagaggg aagagagtga acagaccaag aaaagagaaa aaatccatat acctgaaaga 900
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112 <211> LENGTH: 323
113 <212> TYPE: PRT
114 <213> ORGANISM: Homo sapiens
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120 Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu
121 20 25 30
123 Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val
124 35 40 45
126 Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu
127 50 55 60
129 Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr
130 65 70 75 80
132 Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile
133 85 90 95
135 Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr
136 100 105 110
138 Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala
139 115 120 125
141 Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn

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142      130      135      140
144 Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro
145 145      150      155      160
147 Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr
148      165      170      175
150 Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp
151      180      185      190
153 Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met
154      195      200      205
156 Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser
157      210      215      220
159 Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Ile
160 225      230      235      240
162 Pro Trp Ile Thr Ala Val Leu Pro Thr Val Ile Ile Cys Val Met Val
163      245      250      255
165 Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys Lys Arg Pro Arg Asn
166      260      265      270
168 Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu Arg Glu Glu Ser Glu Gln
169      275      280      285
171 Thr Lys Lys Arg Glu Lys Ile His Ile Pro Glu Arg Ser Asp Glu Ala
172      290      295      300
174 Gln Arg Val Phe Lys Ser Ser Lys Thr Ser Ser Cys Asp Lys Ser Asp
175 305      310      315      320
177 Thr Cys Phe
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182 <211> LENGTH: 834
183 <212> TYPE: DNA
184 <213> ORGANISM: Homo sapiens
186 <400> SEQUENCE: 4
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188 gaaccaccca ctgcatgcag agaaaaacag tacctaataa acagtcagtg ctgttctttg 120
189 tgccagccag gacagaaact ggtgagtgac tgcacagagt tcaactgaaac ggaatgcctt 180
190 ccttgcggtg aaagcgaatt cctagacacc tggaacagag agacacactg ccaccagcac 240
191 aaatactgcg accccaacct agggcttcgg gtccagcaga agggcacctc agaaacagac 300
192 accatctgca cctgtgaaga aggctggcac tgtacgagtg aggcctgtga gagctgtgtc 360
193 ctgcaccgct catgctcgcc cggctttggg gtcaagcaga ttgctacagg ggtttctgat 420
194 accatctgcg agccctgccc agtcggcttc ttctccaatg tgtcatctgc tttcgaaaaa 480
195 tgtcaccctt ggacaagctg tgagaccaa gacctggttg tgcaacaggc aggcacaaac 540
196 aagactgatg ttgtctgtgg tccccaggat cggctgagag ccctggtggt gatccccatc 600
197 atcttcggga tcctgtttgc cactctcttg gtgctggtct ttatcaaaaa ggtggccaag 660
198 aagccaacca ataaggcccc ccacccaag caggaacccc aggagatcaa ttttcccgcg 720
199 gatcttctcg gctccaacac tgctgtctca gtgcaggaga ctttacatgg atgccaaccg 780
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203 <210> SEQ ID NO: 5
204 <211> LENGTH: 277
205 <212> TYPE: PRT
206 <213> ORGANISM: Homo sapiens
208 <400> SEQUENCE: 5
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210      1          5          10          15
212 Ala Val His Pro Glu Pro Pro Thr Ala Cys Arg Glu Lys Gln Tyr Leu
213              20          25          30
215 Ile Asn Ser Gln Cys Cys Ser Leu Cys Gln Pro Gly Gln Lys Leu Val
216              35          40          45
218 Ser Asp Cys Thr Glu Phe Thr Glu Thr Glu Cys Leu Pro Cys Gly Glu
219              50          55          60
221 Ser Glu Phe Leu Asp Thr Trp Asn Arg Glu Thr His Cys His Gln His
222              65          70          75          80
224 Lys Tyr Cys Asp Pro Asn Leu Gly Leu Arg Val Gln Gln Lys Gly Thr
225              85          90          95
227 Ser Glu Thr Asp Thr Ile Cys Thr Cys Glu Glu Gly Trp His Cys Thr
228              100          105          110
230 Ser Glu Ala Cys Glu Ser Cys Val Leu His Arg Ser Cys Ser Pro Gly
231              115          120          125
233 Phe Gly Val Lys Gln Ile Ala Thr Gly Val Ser Asp Thr Ile Cys Glu
234              130          135          140
236 Pro Cys Pro Val Gly Phe Phe Ser Asn Val Ser Ser Ala Phe Glu Lys
237 145          150          155          160
239 Cys His Pro Trp Thr Ser Cys Glu Thr Lys Asp Leu Val Val Gln Gln
240              165          170          175
242 Ala Gly Thr Asn Lys Thr Asp Val Val Cys Gly Pro Gln Asp Arg Leu
243              180          185          190
245 Arg Ala Leu Val Val Ile Pro Ile Ile Phe Gly Ile Leu Phe Ala Ile
246              195          200          205
248 Leu Leu Val Leu Val Phe Ile Lys Lys Val Ala Lys Lys Pro Thr Asn
249              210          215          220
251 Lys Ala Pro His Pro Lys Gln Glu Pro Gln Glu Ile Asn Phe Pro Asp
252 225          230          235          240
254 Asp Leu Pro Gly Ser Asn Thr Ala Ala Pro Val Gln Glu Thr Leu His
255              245          250          255
257 Gly Cys Gln Pro Val Thr Gln Glu Asp Gly Lys Glu Ser Arg Ile Ser
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261              275
264 <210> SEQ ID NO: 6
265 <211> LENGTH: 735
266 <212> TYPE: PRT
267 <213> ORGANISM: Homo sapiens
269 <400> SEQUENCE: 6
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273 Ala Ser Gln Ala Phe Lys Ile Glu Thr Thr Pro Glu Ser Arg Tyr Leu
274              20          25          30
276 Ala Gln Ile Gly Asp Ser Val Ser Leu Thr Cys Ser Thr Thr Gly Cys
277              35          40          45
279 Glu Ser Pro Phe Phe Ser Trp Arg Thr Gln Ile Asp Ser Pro Leu Asn
280              50          55          60
282 Gly Lys Val Thr Asn Glu Gly Thr Thr Ser Thr Leu Thr Met Asn Pro

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283	65				70					75					80	
285	Val	Ser	Phe	Gly	Asn	Glu	His	Ser	Tyr	Leu	Cys	Thr	Ala	Thr	Cys	Glu
286					85					90					95	
288	Ser	Arg	Lys	Leu	Glu	Lys	Gly	Ile	Gln	Val	Glu	Ile	Tyr	Ser	Phe	Pro
289				100					105					110		
291	Lys	Asp	Pro	Glu	Ile	His	Leu	Ser	Gly	Pro	Leu	Glu	Ala	Gly	Lys	Pro
292				115					120					125		
294	Ile	Thr	Val	Lys	Cys	Ser	Val	Ala	Asp	Val	Tyr	Pro	Phe	Asp	Arg	Leu
295				130					135					140		
297	Glu	Ile	Asp	Leu	Leu	Lys	Gly	Asp	His	Leu	Met	Lys	Ser	Gln	Glu	Phe
298	145					150					155				160	
300	Leu	Glu	Asp	Ala	Asp	Arg	Lys	Ser	Leu	Glu	Thr	Lys	Ser	Leu	Glu	Val
301				165						170					175	
303	Thr	Phe	Thr	Pro	Val	Ile	Glu	Asp	Ile	Gly	Lys	Val	Leu	Val	Cys	Arg
304				180						185					190	
306	Ala	Lys	Leu	His	Ile	Asp	Glu	Met	Asp	Ser	Val	Pro	Thr	Val	Arg	Gln
307				195					200					205		
309	Ala	Val	Lys	Glu	Leu	Gln	Val	Tyr	Ile	Ser	Pro	Lys	Asn	Thr	Val	Ile
310				210					215					220		
312	Ser	Val	Asn	Pro	Ser	Thr	Lys	Leu	Gln	Glu	Gly	Gly	Ser	Val	Thr	Met
313	225					230					235				240	
315	Thr	Cys	Ser	Ser	Glu	Gly	Leu	Pro	Ala	Pro	Glu	Ile	Phe	Trp	Ser	Lys
316				245						250					255	
318	Lys	Leu	Asp	Asn	Gly	Asn	Leu	Gln	His	Leu	Ser	Gly	Asn	Ala	Thr	Leu
319				260						265					270	
321	Thr	Leu	Ile	Ala	Met	Arg	Met	Glu	Asp	Ser	Gly	Ile	Tyr	Val	Cys	Glu
322				275					280					285		
324	Gly	Val	Asn	Leu	Ile	Gly	Lys	Asn	Arg	Lys	Glu	Val	Glu	Leu	Ile	Val
325				290					295				300			
327	Gln	Glu	Lys	Pro	Phe	Thr	Val	Glu	Ile	Ser	Pro	Gly	Pro	Arg	Ile	Ala
328	305					310					315				320	
330	Ala	Gln	Ile	Gly	Asp	Ser	Val	Met	Leu	Thr	Cys	Ser	Val	Met	Gly	Cys
331				325						330					335	
333	Glu	Ser	Pro	Ser	Phe	Ser	Trp	Arg	Thr	Gln	Ile	Asp	Ser	Pro	Leu	Ser
334				340					345					350		
336	Gly	Lys	Val	Arg	Ser	Glu	Gly	Thr	Asn	Ser	Thr	Leu	Thr	Leu	Ser	Pro
337				355					360					365		
339	Val	Ser	Phe	Glu	Asn	Glu	His	Ser	Tyr	Leu	Cys	Thr	Val	Thr	Cys	Gly
340				370									380			
342	His	Lys	Lys	Leu	Glu	Lys	Gly	Ile	Gln	Gly	Glu	Leu	Tyr	Ser	Phe	Pro
343	385					390					395				400	
345	Arg	Asp	Pro	Glu	Ile	Glu	Met	Ser	Gly	Gly	Leu	Val	Asn	Gly	Ser	Ser
346				405						410					415	
348	Cys	Thr	Val	Ser	Cys	Lys	Val	Pro	Ser	Val	Tyr	Pro	Leu	Asp	Arg	Leu
349				420					425					430		
351	Glu	Ile	Glu	Leu	Leu	Lys	Gly	Glu	Thr	Ile	Leu	Glu	Asn	Ile	Glu	Phe
352				435					440					445		
354	Leu	Glu	Asp	Thr	Asp	Met	Lys	Ser	Leu	Glu	Asn	Lys	Ser	Leu	Glu	Met
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VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number

E:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date